

## PATENT

Customer No. 22,852

Application No. 09/881,748

Attorney Docket No. 04853.0074-00000

Similarly, amended claim 3 recites analyzing the DNA methylation pattern of gene regions of various types of cell, tissue or nucleus, and comparing them in order to identify gene regions characterizing different types of cell, tissue or nucleus. This finds support in the specification at pages 8-9, for example, which describes analyzing DNA methylation patterns of "specific gene regions" (page 8, line 11) for different cell types, and comparing them (page 9, line 13) in order to determine cell/tissue-specificity. Amended claim 3 is further supported in the specification at pages 18-19, which describes analyzing DNA methylation of several mouse cells and tissues (page 18, lines 17-18), determining positions where the patterns differ depending on cell/tissue-type (page 19, lines 4-6) and thus identifying cell/tissue-specific gene regions (page 19, lines 15-16). See also, page 19, lines 7-11, listing examples of regions with methylation patterns specific to certain cells and tissues; and page 19, lines 27-29, providing four examples of tissue-specific demethylated genes.

Finally, new claim 5, directed to assessing the development of a cell, tissue or nucleus finds support in the specification, for example, at page 9, lines 24-26, which teach how to assess whether a cell is an "undifferentiated embryonic stem cell" or a "differentiated embryonic stem cell;" and further at page 13, lines 25-26, which describe "evaluating the degree of stem cells."

Thus, there is no issue of new matter with respect to new claim 5 and amended claims 1 and 3. Accordingly, claims 1, 3-5 are now pending.

FINNEGAN  
HENDERSON  
FARABOW  
GARRETT &  
DUNNER LLP

1300 I Street, NW  
Washington, DC 20005  
202.408.4000  
Fax 202.408.4400  
www.finnegan.com

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Furthermore, Applicants respectfully request that amended claim 3 and new claim 5 be examined with Group I of the Examiner's telephonic restriction requirement of September 16, 2002. Group I, containing original claim 1, allegedly corresponds to a method of identifying a cell, tissue or nucleus based on its methylation characteristics. Amended claim 3 is directed to identifying gene regions characterizing a type of cell, tissue or nucleus based its methylation characteristics. Thus, amended claim 3 can be included in Group I. And new claim 5 is directed to assessing the development of a cell, tissue or nucleus based on its methylation characteristics. Thus, new claim 5 can also be included in Group I.

If there is any fee due in connection with the filing of this Statement, please charge the fee to our Deposit Account No. 06-0916.

Respectfully submitted,

FINNEGAN, HENDERSON, FARABOW,  
GARRETT & DUNNER, L.L.P.

Dated: October 23, 2002

By: Rebecca M. McNeil  
for Jean B. Fordis Reg. No. 43,796  
Reg. 32,984

FINNEGAN  
HENDERSON  
FARABOW  
GARRETT &  
DUNNER LLP

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Washington, DC 20005  
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APPENDIX

1. (Amended) A method of identifying a cell, tissue or nucleus, comprising:  
  
[collecting information on] analyzing the DNA methylation pattern of [DNA isolated from said] the cell, tissue or nucleus [and];  
  
analyzing the [resultant information] DNA methylation pattern of one or more known types of the cell, tissue or nucleus, and;  
  
comparing the DNA methylation pattern of the cell, tissue or nucleus with the DNA methylation pattern of the one or more known types of cell, tissue or nucleus.  
  
thereby identifying the cell, tissue or nucleus.
3. (Amended) A method of [specifying] identifying one or more gene regions [indispensable for producing] characterizing a type of cell, tissue or nucleus [of interest], comprising:  
  
[using information on] analyzing the DNA methylation pattern of [DNA isolated from a test] one or more gene regions of two or more types of cell, tissue or nucleus [as an indicator], and;  
  
comparing the DNA methylation pattern of the one or more gene regions of two or more types of cell, tissue or nucleus.

FINNEGAN  
HENDERSON  
FARABOW  
GARRETT &  
DUNNER LLP

1300 I Street, NW  
Washington, DC 20005  
202.408.4000  
Fax 202.408.4400  
www.finnegan.com

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
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thereby identifying the one or more gene regions characterizing the type of cell,  
tissue or nucleus.

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FARABOW  
GARRETT &  
DUNNER 

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Fax 202.408.4400  
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